

IWBBIO 2016

INTERNATIONAL WORK-CONFERENCE ON
BIOINFORMATICS AND
BIOMEDICAL ENGINEERING

PROGRAM

20-22 April, 2016
Granada (SPAIN)

Wednesday, April 20, 2016		
8:00-8:30	REGISTRATION DESK <i>(start at 8h but it is opened during all the conference)</i>	
8:30-10:00	Session A.1: Tools for Next Generation Sequencing data analysis	Session B.1: Human Behavior Monitoring, Analysis and Understanding (HBMAU)
10:00-10:30	COFFEE BREAK	
10:30-11:30	OPENING PLENARY LECTURE Prof. Andreas Bender	
11:30-13:00	Session A.2: Using quantitative systems pharmacology for novel drug discovery: a 'systems-level' perspective to reduce toxicity and increase the therapeutic effect of drugs towards 'precision medicine' (Part I)	Session B.2: Advances in Drug Discovery
13:00-15:00	LUNCH & COFFEE	
15:00-16:00	Session A.3: Using quantitative systems pharmacology for novel drug discovery: a 'systems-level' perspective to reduce toxicity and increase the therapeutic effect of drugs towards 'precision medicine' (Part II)	Session B.3: Towards an effective telemedicine: an interdisciplinary approach
16:00-17:30	Session A.4: Next generation sequencing and sequence analysis	Session B.4: Biomedical image analysis (Part I)
17:30-18:30	Session A.5/B.5: Poster Session I	
19:30	Gala Dinner at Hotel Alhambra Palace	

NOTES:

- All **Sessions A** will be held in Salón de Grados, Edificio Mecenas (just 20 meters from the Facultad de Ciencias).
- All **Sessions B** will be held in Salón de Grados, Facultad de Ciencias.
- The **Poster Sessions** will be held in the Hall of Facultad de Ciencias.
- Social event (departure): Buses will be at the main entrance of Hotel Granada Center.

Thursday, April 21, 2016		
8:00-10:00	Session A.6: Computational systems for modelling biological processes	Session B.6: Bioinformatics for healthcare and diseases
10:00-10:30	COFFEE BREAK	
10:30-11:30	PLENARY LECTURE Prof. Ferran Sanz	
11:30-13:00	Session A.7: High Performance Computing in Bioinformatics, Computational Biology and Computational Chemistry (Part I)	Session B.7: Computational proteomics
13:00-15:00	LUNCH & COFFEE	
15:00-16:00	Session A.8: High Performance Computing in Bioinformatics, Computational Biology and Computational Chemistry (Part II)	Session B.8: Biomedical image analysis (Part II)
16:00-17:45	Session A.9: Resources for bioinformatics	Session B.9: Fundamentals of biological dynamics and maximization of the information extraction from the experiments in the biological systems
17:45-18:45	Session A.10/B.10: Poster Session II	
19:30	Light dinner at the Carmen de los Martires	

Friday, April 22, 2016		
8:00-10:00	Session A.11: Pattern Recognition and Machine Learning in the -omics sciences	Session B.11: Assistive Technology for People with Neuromotor Disorders
10:00-10:30	COFFEE BREAK	
10:30-11:30	CLOSING PLENARY LECTURE Prof. Rita Casadio	
11:30-13:30	Session A.12: Biomedical signal analysis	Session B.12: Advanced in computational biology
13:30-15:30	LUNCH & COFFEE	
16:15	Visit to the Alhambra	

IWBBIO 2016 FULL PROGRAM

Wednesday, April 20, 2016

Session A.1: "Tools for Next Generation Sequencing data analysis"

Chairman: Dr. Gonzalo Claros and Dr. Javier Perez

Automatic workflow for the identification of constitutively-expressed genes based on NGS reads mapping

Rosario Carmona, Pedro Seoane, Adoración Zafra, María José Jiménez-Quesada, Juan De Dios Alché and Gonzalo Claros

Prioritization of schizophrenia risk genes by a network-regularized logistic regression method

Wen Zhang, Jhin-Rong Lin, Rubén Nogales-Cadenas, Quanwei Zhang, Ying Cai and Zhengdong Zhang

GNATY: Optimized NGS variant calling and coverage analysis

Beat Wolf, Pierre Kuonen and Thomas Dandekar

Rational confederation of genes and diseases: NGS interpretation via GeneCards, MalaCards and VarElect

Noa Rappaport, Michal Twik, Frida Belinky, Inbar Plaschkes, Gil Stelzer, Ron Nudel, Tsippi Iny Stein, Danit Oz-Levi, Dana Cohen, Simon Fishilevich, Marilyn Safran and Doron Lancet

Session B.1: "Human Behavior Monitoring, Analysis and Understanding (HBMAU)"

Chairman: Dr. Orestí Baños and Dr. Hector Pomares

Consistency verification of marker-less gait assessment system for stair walking

Ami Ogawa, Ayanori Yorozu, Akira Mita, Masaki Takahashi, Christos Georgoulas and Thomas Bock

Full Body Gesture Recognition for Human-Machine Interaction in Intelligent Spaces

David Casillas-Perez, Javier Macias-Guarasa, Marta Marron-Romera, David Fuentes-Jimenez and Alvaro Fernandez-Rincon

A Web System for Managing and Monitoring Smart Environments

Daniel Zafra, Javier Medina Quero, Luis Martinez, Chris Nugent and Macarena Espinilla

A Sequential Kalman Filter Approach for Estimation of Human Body Orientation Based on Body-attached IMMU Signals

Jung Keun Lee

A platform for enhancing the Epilepsy Anamnesis

Enrique De La Cal Marín, José Ramón Villar, Javier Sedano, Manuel Menéndez, Paula Vergara and Victor González

High-Level Context Architecture for Real Time Identification of Human Behavior

Claudia Villalonga, Oresti Banos, Hector Pomares, Ignacio Rojas and Sungyoung Lee

OPENING PLENARY LECTURE:

Dr. Andreas Bender

Department of Chemistry. Centre for Molecular
Informatics. Bender Group.
University of Cambridge.

Session A.2: "Using quantitative systems pharmacology for novel drug discovery: a 'systems-level' perspective to reduce toxicity and increase the therapeutic effect of drugs towards 'precision medicine' (Part I)"

Chairman: Dr. Violeta I. Perez-Nueno

A general view of computational methods for target fishing and focus on the use of fingerprints for chemical similarity searching

Adrià Ceretó-Massagué, María José Ojeda, Aleix Gimeno, Sarah Tomás-Hernández, Cristina Valls, Raul Beltrán-Debón, Miquel Mulero, Gerard Pujadas and Santi Garcia-Vallve

Relating drugs targets and side effects using GES and GESSE

Violeta Isabel Perez Nueno

Exploiting Systems Pharmacology in Cancer Therapeutics

Albert Antolin, Paul Clarke, Paul Workman and Bissan Al-Lazikani

In silico drug-repurposing analysis for T Lymphocytes of Systemic Lupus Erythematosus

Daniel Toro Dominguez, Pedro Carmona Saez and Marta Eugenia Alarcon Riquelme

Network analysis of drug toxicity proteins and the impact of likely deleterious variation

Janet Piñero and Laura I. Furlong

Integration of Structured and Unstructured Data for Target and Lead Discovery

John Overington

Session B.2: "Advances in Drug Discovery"

Chairman: Dr. Horacio Pérez-Sánchez, Dr. Alfonso Pérez-Garrido and Dr. José Pedro Cerón

Innovative biomarker-based clinical trial designs

Chul Ahn

Predicted protein-protein interaction in TRKB complex using multiple open tools to drive experimental data

Plinio Casarotto, Senem Merve Oztas, Caroline Biojone, Liisa Vesa, Juzoh Umemori, Markku Varjosalo, Helka Nukkala, Tomi Rantamaki and Eero Castren

Biological Activities of Actinomycetes Isolated from Saudi Marine Habitats for Disease Control

Wael Hozzein, Sameh Khalaf and Mohammed Wadaan

Identification of Novel Trypanosoma Cruzi Prolyl Oligopeptidase Inhibitors by Structure-Based Virtual Screening

Izabela Marques Dourado Bastos, Hugo de Almeida, Flávia Nader Motta, Vincent Leroux, Philippe Grellier, Bernard Maigret and Jaime Martins Santana

HYDROWEB, an online tool for the calculation of hydrodynamic properties of macromolecules

Horacio Pérez-Sánchez, Jorge Peña-García, Helena Den-Haan, Ricardo Rodríguez-Schmidt, José P. Cerón-Carrasco, Adriano N. Raposo, Mounira Bouarkat, Sid Ahmed Sabeur and Francisco Guillermo Díaz-Baños

Non-steroidal anti-inflammatory drugs as inhibitors of cyclooxygenases: what we have learned and what is next

Jose Pedro Ceron-Carrasco, Jorge de La Peña and Horacio Perez-Sanchez

Session A.3: "Using quantitative systems pharmacology for novel drug discovery: a 'systems-level' perspective to reduce toxicity and increase the therapeutic effect of drugs towards 'precision medicine' (Part II)"

Chairman: Dr. Violeta I. Perez-Nueno

Drug Profile Matching: Drug Discovery by Polypharmacology-based Interaction Profiling

Zoltan Simon, Agnes Peragovics, Anna Rauscher, Balazs Jelinek, Pal Czobor, Istvan Bitter, Peter Hari and Andras Malnasi-Csizmadia

Network based Drug Repositioning Methodology for Neuro-degenerative Diseases

Mingmei Shang, Narsis Kiani and Jesper Tegner

Tools for Medicinal Chemistry navigation

Obdulia Rabal and Julen Oyarzabal

Session B.3: "Towards an effective telemedicine: an interdisciplinary approach"

Chairman: Dr. Maria Francesca Romano

CentoMD®, the largest variant database for rare diseases

Daniel Trujillano

Use of Mobile Application for Nutrition Health Education

Hsiao-Hui Li, Mei-Hua Lo and Yuan-Hsun Liao

Proving experiment of international virtual slide telepathology, Japan-Vietnam, China, and Myanmar trials

Ichiro Mori and Yoshiyuki Osamura

Session A.4: "Next generation sequencing and sequence analysis"

Chairman: Dr. Zhang Zhengdong and Dr. Noa Rappaport

Different approaches and automatic decision to obtain a high quality 'de novo' transcriptome for *Castanea sativa*

Marina Espigares, Pedro Seoane, Rocío Bautista, Julia Quintana, Isabel Gonzalez, Luis Gomez and M. Gonzalo Claros

Adapting GECKO for metagenomics studies

Fernando Moreno Jabato, Oswaldo Trelles Salazar and Óscar Torreño Tirado

Algorithms of NGS data evaluation in patients with Parkinsonism from genetically isolated population

Radek Vrtel, Radek Vodicka, Katerina Mensikova, Petr Kanovsky, Iva Dolinova, Kristyna Kolarikova and Martin Prochazka

Airway transcriptome analysis in a model of asthma reveals impaired homeostasis and tissue repair

Laurence Tessier, Olivier Côté, Mary-Ellen Clark, Laurent Viel, Andres Diaz-Méndez, Simon Anders and Dorothee Bienzle

De novo Assembly and Cluster Analysis of Siberian Larch Transcriptome and Genome

Michael Sadovsky, Konstantin Krutovsky, Natalia Oreshkova, Julia Putintzeva, Vladislav Birukov and Serafima Novikova

Session B.4: "Biomedical image analysis (Part I)"

Chairman: Dr. Noborio Hiroshi and Dr. Ignacio Rojas

Uncertainty in 1D and 3D Models of a Fiber Stimulated by an External Electrode

Wanda Krassowska Neu

Tracking a Real Liver using a Virtual Liver and an Experimental Evaluation with Kinect v2

Hiroshi Noborio, Kaoru Watanabe, Masahiro Yagi, Yasuhiro Ida, Shigeki Nankaku, Katsuhiko Onishi, Masanao Koeda, Masanori Kon, Kosuke Matsui and Masaki Kaibori

Thermal Imaging-Based Muscular Activity in the Biomechanical Study of Surgeons

Ramon Sancibrian, Maria C. Gutierrez-Diez, Carlos Redondo-Figuero, Esther G. Sarabia, Maria A. Benito-Gonzalez and Jose C. Manuel-Palazuelos

FCM-based method for MRI segmentation of anatomical structure

Antonio Pinti

Session A.5/B.5: "Poster Session (Part I)"

Chairman: Dr. Olga Valenzuela and Dr. Fernando Rojas

Interaction of miRNAs with cell cycle genes mRNAs

Raigul Niyazova, Shara Atambayeva, Aigul Akimniyazova and Anatoly Ivashchenko

Detection of 3D coordinates in fish shoal behavior monitoring: comparison of methods

Aliaksandr Pautsina and Petr Císar

feature selection and detection of Liver Disorders using neuro-genetic approach

Mansouria Sekkal and Mohamed Amine Chikh

Crucial nutrients in complex system environment

Pavel Soucek, Antonin Barta, Petr Cisar and Petr Tuma

Probing binding hot spots at protein–RNA recognition sites

Amita Barik, Chandran Nithin, Naga Bhushana Rao Karampudi, Sunandan Mukherjee and Ranjit Prasad Bahadur

A mathematical model for the accurate prediction of protein-RNA binding affinity using structural and physiochemical parameters

Chandran Nithin, Sunandan Mukherjee and Ranjit Prasad Bahadur

Automating water flow estimation in fish tanks

Petr Císar, Movchan Oleksandr, Jaroslav Hanak and Antonin Barta

Inter-observer reliability and agreement study on early diagnosis of diabetic retinopathy and diabetic macular edema risk

Manuel Emilio Gegundez-Arias, Carlos Ortega, Javier Garrido, Beatriz Ponte, Fatima Alvarez and Diego Marin

Automated detection of diabetic macular edema risk in fundus images

Diego Marin, Manuel Emilio Gegundez-Arias, Carlos Ortega, Javier Garrido, Beatriz Ponte and Fatima Alvarez

Hydration of protein-RNA recognition sites

Amita Barik and Ranjit Prasad Bahadur

The Pulsatile Flow Feature Investigation through Stenotic Tube based on Angiogram

Ho Seong Ji

Managing hypertension with an app based on an antihypertensive dash diet.

Jose Manuel Alcaide Leyva, Leticia Capelo Sanchís, Guillermo Molina Recio, Laura García-Hernández and Rafael Molina Luque

Inhibition of Bone Resorption by Suppressing Osteoclast Differentiation via Gold-nanoparticles Combined Drug

Donghyun Lee, Dong Nyoungh Heo, Sang Jin Lee and Il Keun Kwon

Performance Benchmarking and Analysis of Bioinformatics Pipelines At Scale

Gaurav Kaul, Serge Osokin and Nagarajan Kathiresan

Extraction of linear separating keys from clinical and genetic data sets

Leon Bobrowski

A Framework for The Disease Trajectory Data Warehouse Conceptual Modeling Support

Mouhamed Gaith Ayadi, Riadh Bouslimi and Jalel Akaichi

Computing EFM's using balanced subgraphs and boolean logic

José Francisco Hidalgo Céspedes, Francisco De Asís Guil Asensio and Jose Manuel García Carrasco

Confluence of Genes Related to the Combined Etiology DOISm (Diabetes, Obesity, Inflammation and Metabolic Syndrome) in Dissecting Nutritional Phenotypes

Ana Paula Moreira Bezerra, Samara Cardoso Silva-Santiago, Jose Francisco Diogo Da Silva Junior, Emanuel Diego S. Penha, Monalisa M Silveira, Myrna S Ramos, Mônica M Silva, Ana Carolina L Pacheco and Diana Magalhaes Oliveira

Comparison of Statistical and Artificial Intelligence-based Classification Methods on Brain Cancer Microarray Gene Expression Data

Mustafa Turan Arslan and Adem Kalinli

Fuzzy vs Kmeans clustering in QSAR data partition. A comparative study.

Francisco Girón-Rodríguez, Alfonso Pérez-Garrido, Horacio Pérez-Sánchez and Jesus Soto

Structure and Interaction Analysis of Buffalo Prolactin (buPRL) By In Silico Approaches

Kailash Prajapati, Pratishtha Singh, Kambadur Muralidhar and Sudha Cowsik

A Universal Sign Language to Voice Translator

Waleed Alshaibani, Abdullah Migdadi and Husam Hamad

Improving knowledge extraction from gene enrichment analysis

Aurelio Lopez-Fernandez, Domingo S. Rodriguez-Baena and Francisco A. Gomez-Vela

A National Genome Research Architecture

Teemupekka Virtanen and Qin Zhang

Electrophysiological measurement of effects of color over level of stress

Diego Adrián Renedo, Miguel Ángel López, Jesús Minguillón and Francisco Pelayo

Studying the herd immunity effect of the varicella vaccine in the Community of Valencia, Spain

Ana Díez-Gandía, Rafael-J. Villanueva, José-A. Morano, Luis Acedo, Juan Mollar and Javier Díez-Domingo

Modelling stroke disease combining Markov processes and the random variable transformation method

Juan Carlos Cortés López, Ana Navarro Quiles, Jose Vicente Romero Bauset and Maria Dolores Roselló Ferragud

Analysing OMIM disease-related variations: a large-scale investigation at the chromosome level

Giulia Babbi, Pier Luigi Martelli, Giuseppe Profiti and Rita Casadio

Rational confederation of genes and diseases: NGS interpretation via GeneCards, MalaCards and VarElect

Noa Rappaport, Michal Twik, Frida Belinky, Inbar Plaschkes, Gil Stelzer, Ron Nudel, Tsippi Iny Stein, Danit Oz-Levi, Dana Cohen, Simon Fishilevich, Marilyn Safran and Doron Lancet

Role of Optical Sensors in Precision Aquaculture

Mohammadmehdi Saberioon and Petr Cisar

Clustering of multi-image sets using Rényi information entropy

Renata Rychtarikova and Dalibor Stys

Least Information Loss (LIL) Conversion of Digital Images and Lessons Learned for Scientific Image Inspection

Dalibor Stys, Tomas Nahlik, Petr Machacek, Renata Rychtářiková and Mohammadmehdi Saberioon

The Image Explorer software: tool for visual exploration of image information content

Petr Machacek, Petr Cisar, Tomas Nahlik, Renata Rychtarikova and Dalibor Stys

Inferring Human Behavior by means of Multimodal Context Mining

Oresti Banos, Claudia Villalonga, Bang Jaehun, Hur Tae-ho, Kang Donguk, Park Sangbeom, Thien Huynh-The, Vui Le-Ba and Sungyoung Lee

Identifying human genetic variants in next-generation sequencing datasets

Joana Tavares, Maria Carmo Fonseca and Ana Rita Grosso

Thursday, April 21, 2016

Session A.6: "Computational systems for modelling biological processes"

Chairman: Dr. Chun-Wei Tung and Dr. Rodrigo Weber dos Santos

Prediction of proinflammatory potentials of engine exhausts by integrating chemical and biological features

Chia-Chi Wang, Ying-Chi Lin, Yuan-Chung Lin, Syu-Ruei Jhang and Chun-Wei Tung

Calculating Elementary Flux Modes with Variable Neighbourhood Search

Jose A. Egea and José Manuel García

Using Nets-Within-Nets for Modeling Differentiating Cells in the Epigenetic Landscape

Roberta Bardini, Alfredo Benso, Stefano Di Carlo, Gianfranco Politano and Alessandro Savino

Simulations of cardiac electrophysiology combining GPU and adaptive mesh refinement algorithms

Rafael S. Oliveira, Bernardo M. Rocha, Denise Burgarelli, Wagner Meira Jr and Rodrigo W. Dos Santos

Modeling dependence in multistate processes

Gregorio Rubio, María Belén García Mora, Cristina Santamaria and José Luis Pontones

A plasma flow model in the interstitial tissue due to bacterial infection

Ruy Freitas Reis, Rodrigo Weber Dos Santos and Marcelo Lobosco

Reactive Interstitial and Reparative Fibrosis as Substrates for Cardiac Ectopic Pacemakers and Reentries

Rafael Sachetto Oliveira, Bruno Gouvea de Barros, Johnny Moreira Gomes, Marcelo Lobosco, Sergio Alonso, Markus Baer and Rodrigo Weber Dos Santos

Session B.6: "Bioinformatics for healthcare and diseases"

Chairman: Dr. Julian Gardner and Dr. Bing Wang (To be confirmed)

Development of a handheld side-stream breath analyser for point of care metabolic rate measurement

Tim Vincent, Julian Gardner, Adrian Wilson, John Hattersley and Mike Chappell

Transcriptome-based identification of a seed olive legumin (11S globulin).

Characterization of subunits, 3D modelling and molecular assessment of allergenicity

Adoración Zafra, Jose Carlos Jimenez-Lopez, Rosario Carmona, Gonzalo Claros and Juan De Dios Alche

A Feature Selection Scheme for Accurate Identification of Alzheimer's Disease

Bing Wang

Comparative analysis of microRNA-target gene interaction prediction algorithms - the attempt to compare the results of three algorithms

Anna Krawczyk and Joanna Polanska

A novel divisive iK-means algorithm with region-driven feature selection as a tool for automated detection of tumour heterogeneity in MALDI IMS experiments

Grzegorz Mrukwa, Grzegorz Drazek, Monika Pietrowska, Piotr Widlak and Joanna Polanska

Multigene p-value integration based on SNPs investigation for seeking radiosensitivity signatures

Joanna Zyla, Christophe Badie, Ghazi Alsbeih and Joanna Polanska

Epithelial Mesenchymal Transition Regulatory Network-based Feature Selection in Lung Cancer Prognosis Prediction

Borong Shao and Tim Conrad

PLENARY LECTURE:

Prof. Ferran Sanz

Director, Research Programme on Biomedical Informatics (GRIB)
Hospital del Mar Medical Research Institute (IMIM) Dept. of
Health and Life Sciences, Universitat Pompeu Fabra

Session A.7: "High Performance Computing in Bioinformatics, Computational Biology and Computational Chemistry (Part I)"

Chairman: *Dr. Horacio Pérez-Sánchez and Dr. Jose M. Cecilia*

The Case for Docker in multicloud enabled bioinformatics applications

Ahmed Abdullah Ali, Mohamed El-Kalioby and Mohamed Abouelhoda

Flexible protein-peptide docking with knowledge about the binding site using CABS-dock

Mateusz Kurcinski, Maciej Pawel Ciemny, Maciej Blaszczyk, Andrzej Kolinski and Sebastian Kmiecik

Computational Modeling and interaction analysis of cannabinoid receptor interacting protein 1a (CRIP1a) with CB1 receptor

Pratishtha Singh, Allyn Howlett and Sudha Cowsik

Real Time GPU-based Segmentation and Tracking of the Left ventricle on 2D Echocardiography

Sidi Ahmed Mahmoudi, Mohammed Ammar, Guillaume Luque Joris and Amine Abbou

Photosynthesis and Electronic Properties of Fenna-Matthews-Olson Light Harvesting Complexes

Shyam Badu, Roderick Melnik and Sanjay Prabhakar

Session B.7: "Computational proteomics"

Chairman: *Dr. Ranjit Vijayan, Dr. Olga Valenzuela and D. Maciej Ciemny*

Identifying phytochemical inhibitors to target antiapoptotic proteins using molecular docking and simulations

Ranjit Vijayan and Priya Antony

From protein variations to biological processes and pathways with NET-GE

Samuele Bovo, Pietro Di Lena, Pier Luigi Martelli, Piero Fariselli and Rita Casadio

Mapping of RNA binding residues in human proteome using global and local protein sequence features

Srinivasan Sivanandan, Chandran Nithin, Sunandan Mukherjee and Ranjit Prasad Bahadur

Towards protein-protein docking with significant structural changes using CABS-dock

Maciej Ciemny, Mateusz Kurcinski, Andrzej Kolinski and Sebastian Kmiecik

AC-DIAMOND: Accelerating Protein Alignment via Better SIMD Parallelization and Space-Efficient Indexing

Huijun Mai, Dinghua Li, Yifan Zhang, Henry Chi-Ming Leung, Ruibang Luo, Hingfung Ting and Tak-Wah Lam

Session A.8: "High Performance Computing in Bioinformatics, Computational Biology and Computational Chemistry (Part II)"

Chairman: *Dr. Horacio Pérez-Sánchez and Dr. Jose M. Cecilia*

Parallel Ant Colony Optimization for the HP Protein Folding Problem

Antonio Llanes, Carlos Velez, Antonia M. Sánchez, Horacio Pérez-Sánchez and José M. Cecilia

Neuroimaging registration on GPU: Energy-aware acceleration

Francisco Nurudín Álvarez, José Antonio Cabrera, Juan Francisco Chico, Jesús Pérez and Manuel Ujaldon

Unleashing the Graphic Processing Units-based version of NAMD

Yamandú González, Pablo Ezzatti and Margot Paulino

Session B.8: "Biomedical image analysis (Part II)"

Chairman: *Dr. Antonio Pinti and Dr. Wanda Krassowska Neu*

An Automated Tensorial Classification Procedure for Left Ventricular Hypertrophic Cardiomyopathy

Santiago Sanz-Estébanez, Javier Royuela-Del-Val, Susana Merino-Caviedes, Ana Revilla-Orodea, Teresa Sevilla, Lucilio Cordero-Grande, Marcos Martín-Fernández and Carlos Alberola-López

Depth Image Matching Algorithm for Deforming and Cutting a Virtual Liver via its Real Liver Image Captured using Kinect v2

Hiroshi Noborio, Kaoru Watanabe, Masahiro Yagi, Kentaro Takamoto, Shigeki Nankaku, Katsuhiko Onishi, Masanao Koeda, Masanori Kon, Kosuke Matsui and Masaki Kaibori

Optic Disc Segmentation with Kapur-ScPSO based Cascade Multithresholding

Hasan Koyuncu and Rahime Ceylan

Session A.9: "Resources for bioinformatics"

Chairman: Dr. Pablo Porras and Dr. Rafael Jimenez

ELIXIR, the European life-science infrastructure for biological information and its implementation phase

Rafael C Jimenez

Gene set disease enrichment analysis from literature data

Jean Fontaine and Miguel Andrade-Navarro

The MINTAct archive for mutations influencing molecular interactions

Pablo Porras Millan, Margaret Duesbury, Maximilian Koch, Sandra Orchard and The Imex Consortium Curation Team

DisGeNET: a versatile platform to support biomedical translational research

Janet Piñero, Núria Queralt-Rosinach, Àlex Bravo, Ferran Sanz and Laura I. Furlong

Lightweight Microbiome Analysis Pipelines

Trevor Cickovski, Vanessa Aguiar-Pulido, Wenrui Huang, Shamsed Mahmud and Giri Narasimhan

A novel standardized partial area index under receiver operating characteristic curves with application to genomic studies

Juana-María Vivo, Manuel Franco and Donatella Vicari

Session B.9: "Fundamentals of biological dynamics and maximization of the information extraction from the experiments in the biological systems"

Chairman: Dr. Dalibor Stys and Dr. Jan Urban

Unsupervised probabilistic detection of protein spots in two-dimensional gel electrophoresis

Jan Urban and Dalibor Stys

Processing plugins for protocols extensions

Antonin Barta, Pavel Soucek and Petr Cisar

Effect of Spatial Constraint on the Self-Organizing Behavior of the Belousov-Zhabotinsky Reaction

Anna Zhyrova, Renata Rychtáriková and Tomáš Náhlík

On Optimization of FRAP Experiments: Model-Based Sensitivity Analysis Approach

Stepan Papacek and Stefan Kindermann

Reachability of the Therapeutic Target in the Systems with Parameters Switch

Magdalena Ochab, Krzysztof Puszynski and Andrzej Swierniak

The complexity of some pattern problems in the logical analysis of large genomic data sets

Giuseppe Lancia and Paolo Serafini

Session A.10/B.10: "Poster Session (Part II)"

Chairman: Dr. Ignacio Rojas, Dr. Hector Pomares and Dr. Fernando Rojas

Multiobjective based scoring function for ligand based virtual screening

Savíns Puertas Martín, Helena Den-Haan, Juana López Redondo, Horacio Pérez Sánchez and Pilar Martínez Ortigosa

A mechanistic study of lncRNA Fendrr regulation of FoxF1 lung cancer tumor supressor

Carmen Navarro, Carlos Cano, Marta Cuadros, Antonio Herrera-Merchan, Miguel Molina-Solana and Armando Blanco

Precocious Diagnosis of Preterm Labor Immediacy by Autoregressive Integrated Moving Average Models

Iker Malaina, Roberto Matorras, Luis Fernandez, Carlos Bringas, Larraitx Aranburu, Idefonso De La Fuente Martinez, Itziar Arana and Leire Gonzalez

GECKO-MGV: Evolution Events driven tool for enhanced visual analysis of multi-genome comparisons

Sergio Díaz Del Pino, Jose Antonio Arjona Medina, Oscar Torreño Tirado, Samuel Benavides García and Oswaldo Trelles

Translucency Thresholds in Dental Resin Composites: Preliminary Results

María M Pérez, Marianne Salas, Luis Javier Herrera, Rosa Pulgar, Ana Yebra, Razvan Ghinea and Cristina Lucena

Influence of Normalization on the Analysis of Electroanatomical Maps with Manifold Harmonics

Margarita Sanromán-Junquera, Inmaculada Mora-Jiménez, Arcadio García-Alberola, Antonio Caamaño-Fernandez and José Luis Rojo-Álvarez

Molecular modeling studies of thieno[3,2-c]pyran analogues as inhibitor against the anti-inflammatory target COX-2

Dharmendra Kumar Yadav, Sanjeev Misra, Praveen Sharma, Horacio Pérez-Sánchez, Harpreet Singh and Surendra Kumar

A semantic-based metadata validation for an automated High-Throughput Screening workflow: Case study in CytomicsDB

Enrique Larios Vargas, Zhihan Xia, Joris Slob and Fons Verbeek

Structural Basis for Understanding Functions of Short Linear Motifs: Bioinformatics and Molecular Dynamics Simulation Study

Nurbubu Moldogazieva and Innokenty Mokhosev

Extraction and analysis approach applied to the complementary and alternative medicine

Ghazi Abdelkader Khodjet El Khil, Marwen Landoulsi, Rahma Daikhi and Houssein Khodjet El Khil

A computational survey of approaches for False Localization Rate measurement in post-translational modifications of proteins.

David Ovelheiro and Santos Blanco

Human action recognition in realistic scenes based on Action Bank

Carlos Martínez-García, Marcos Baptista-Ríos, Cristina Losada-Gutiérrez, Marta Marrón-Romera and Valeria Boggian

GrantFinder, a web based tool for the search of research grant calls

Jorge Peña-García, Helena Den-Haan, Alberto Caballero, Baldomero Imbernón, José P. Cerón-Carrasco, Antonio Vicente-Contreras and Horacio Pérez-Sánchez

A hybrid machine learning and molecular modeling methodology for the prediction of novel blood anticoagulants

Ricardo Rodríguez-Schmidt, Jorge Peña-García, Alfonso Pérez-Garrido, Helena Den-Haan, Andrés Bueno-Crespo, José Cerón-Carrasco, Anil Thapa, Jon Atli-Benediktsson, Jesús Soto and Horacio Pérez-Sánchez

ZincFetcher: a tool for easy compound filtering from ZINC database

Jorge Peña-García, Alfonso Pérez-Garrido, Andrés Muñoz, Helena Den-Haan, Baldomero Imbernón, José P. Cerón-Carrasco, Dariusz Mrozek, Anil Thapa, Jesús Soto, Antonio Banegas-Luna and Horacio Pérez-Sánchez

Biomolecular annotation integration and querying to help unveiling new biomedical knowledge

Arif Canakoglu, Stefano Ceri and Marco Masseroli

Usage of AdaBoost Algorithm as a Feature Selection Method and Comparison with Other Feature Selection Algorithms

Mucahid Barstugan and Rahime Ceylan

L. sibirica Lebed. Chloroplast Genome Yields Unusual Seven-Cluster Structure

Michael Sadowsky, Julia Putnzeva, Konstantin Krutovsky, Eugenia Bondar and Natalia Oreshkova

Characterization of the Polymerization Reaction of Dental Nanocomposites by Laser Speckle Patterns

Antonio M Pozo, Ana Yebra, Ana M Ionescu, Juan C Cardona, Francisco Carrillo-Pérez, Razvan Ghinea and María M Pérez

Network ranking assisted semantic data mining

Jan Kralj, Anže Vavpetić, Michel Dumontier and Nada Lavrac

Computer-Assisted Molecular Traceability for Dairy Farming Products

Francesco Rossi, Paola Modesto, Stefano Di Carlo, Gianfranco Politano, Alessandro Savino, Per Luigi Acutis and Alfredo Benso

Audio Enhancement for Vocalization Detection in a Neonatal Intensive Care Unit Environment

Ganna Raboshchuk, Climent Nadeu, Sergio Vidiella Pinto, Oriol Ros Fornells, Blanca Muñoz Mahamud and Ana Riverola de Veciana

Non-invasive measurements of translucency in dental biomaterials

Razvan Ghinea, Cristina Gasparik, Ana Maria Ionescu, Juan De La Cruz Cardona, Diana Dudea and María M Pérez

Analysis of questionnaire-based obstetric data using machine learning approach

Justyna Pieter, Sebastian Student, Karolina Sobczyk and Krzysztof Fajarewicz

Bioactive heterocycles in the leaves essential oil of *cotula cinerea* growing in Algeria desert

Nacéra Tigrine

Rational Design of Highly Potent M. tuberculosis CYP130 Inhibitors: 3D-QSAR study and Molecular Dynamic Simulations

Pijitra Meewong, Pharit Kamsri, Auradee Punkvang, Patchareenart Saparpakorn, Supa Hannongbua, Ubolsree Leartsakulpanich and Pornpan Pungpo

bees Swarm Optimisation for Molecular Docking

Hocine Saadi, Youcef Djanouri, Nadia Nouali, Abd Latif Rahmoun, Malika Mehdi and AHCÈNE Bendjoudi

Determining the relevant 3D regions of the brain for the classification of subjects related to Alzheimer's disease.

Olga Valenzuela and Xiaoyi Jiang

A new approach to improve coping strategies to surgery in children

Alberto Guillen

A Possible Secure Android Web Service Application in SOA Based Mobile Healthcare Systems

Slobodan Bojanic, Milan Markovic and Goran Dordevic

Designing a Gamified System to Support Cancer Patients' Recovery

Salvador Moreno, Miguel Damas, Hector Pomares and Oresti Banos

The feasibility of 3D bioprinting personalised ATMP/device combination products for nasal reconstructive surgery.

Andrew Gleadall

Friday April 22, 2016

Session A.11: Pattern Recognition and Machine Learning in the -omics sciences”

Chairman: Dr. Alfredo Vellido, Dr. Jesus Giraldo and Dr. René Alquézar

Random Forests for quality control in G-Protein Coupled Receptor databases

Aleksei Shkurin and Alfredo Vellido

Automated quality control for proton magnetic resonance spectroscopy data using convex non-negative matrix factorization

Victor Mocioiu, Sreenath P. Kyathanahally, Carles Arús, Alfredo Vellido and Margarida Julià-Sapé

A machine learning methodology for enzyme functional classification combining structural and protein sequence descriptors

Afshine Amidi, Shervine Amidi, Dimitrios Vlachakis, Nikos Paragios and Evangelia Zacharaki

Network-inspired approaches for transcriptomic analyses

Vanessa Aguiar-Pulido, Victoria Suarez-Ulloa, Elizabeth Puente, Wenrui Huang, Jose M. Eirin-Lopez and Giri Narasimhan

Gene-disease Prioritization through Cost-Sensitive Graph-based Methodologies

Marco Frasca and Simone Bassis

A comprehensive comparison of two MEDLINE annotators for disease and gene linkage: sometimes less is more

Sarah Elshal, Jaak Simm, Adam Arany, Pooya Zakeri, Jesse Davis and Yves Moreau

Genetic Algorithms for Unified Design Inference

Jaime Rodríguez-Guerra Pedregal and Jean-Didier Maréchal

Session B.11: ”Assistive Technology for People with Neuromotor Disorders”

Chairman: Dr. Rafael Raya and Dr. Gabriel Caffarena

Sainet: An Image Processing App for Assistance of Visually Impaired People in Social Interaction Scenarios

Jesus Salido, Oscar Deniz and Gloria Bueno

The Effect of Transcranial Direct Current Stimulation (tDCS) over Human the Motor Function

Cristian Pérez-Fernández, Ana Sánchez-Kuhn, Rosa Cánovas, Pilar Flores and Fernando Sanchez-Santed

A study in experimental methods of human-computer communication for patients after severe brain injuries

Andrzej Czyzewski and Bozena Kostek

Evaluation of Cervical Posture Improvement of Children with Cerebral Palsy after Physical Therapy with a HCI Based on Head Movements and Serious Videogames

Miguel A. Velasco, Rafael Raya, Luca Muzzioli, Daniela Morelli, Marco Iosa, Febo Cincotti and Eduardo Rocon

Enriched Environment Affects Positively a Progression of Neurodegeneration: Elastic Maps-Based Analysis

Michael Sadovsky, Andrey Morgun, Alla Salmia, Natalia Kuvacheva, Elena Khilazheva and Elena Pozhilenkova

Muscle coordination during cycling: a new biofeedback approach in neurorehabilitation

Diego Torricelli and Jose Luis Pons

CLOSING PLENARY LECTURE:

Prof. Rita Casadio

Group leader of the Bologna Biocomputing Unit University of Bologna (UNIBO), Bologna (Italy)

Session A.12: "Biomedical signal analysis"

Chairman: Dr. Mario Rosario Guarracino and Dr. Andrzej Czyzewski

Assessing parallel heterogeneous computer architectures for multiobjective feature selection on EEG classification

Juan José Escobar, Julio Ortega, Jesús González and Miguel Damas

A predictive model for surgical planning in breast cancer treatment.

Daniela Evangelista, Marina Piccirillo, Tiziana Ricciardelli, Massimiliano D'Aiuto and Mario Rosario Guarracino

A Comparison of Feature Ranking and Rank Aggregation Techniques in Automatic Sleep Stage Classification based on Polysomnographic Signals

Shirin Najdi, Ali Abdollahi Gharbali and José Manuel Fonseca

Improved dynamic time warping for abnormality detection in ECG time series

Imen Boulnemour, Bachir Boucheham and Slimane Benloucif

Hardware Accelerator to Compute the Embedding Minimum Dimension of ECG Records

Pablo Pérez-Tirador, Gabriel Caffarena, Constantino A. García, Abraham Otero, Rodrigo García and Rafael Raya

Low-power, Low-latency Hermite Polynomial Characterization of Heartbeats using a Field-Programmable Gate Array

Kartik Lakhotia, Gabriel Caffarena, Alberto Gil, David G. Marquez, Abraham Otero and Madhav P. Desai

Session B.12: "Advanced in computational biology"

Chairman: Dr. Michael Sadovsky and Dr. Marco Frasca

Angel: Towards a multi-level method for the analysis of variants in individual genomes

Ginés Almagro Hernández, Francisco Garcia-Sanchez, María Eugenia de La Morena Barrio, Javier Corral de La Calle and Jesualdo Tomás Fernández-Breis

Of text and gene – Analysis of big genomics data with text mining methods

Weida Tong

Constructing a database for the annotation and characterisation of non-coding genomic regions using Ruby

Elena Rojano, Pedro Seoane-Zonjic, Juan Antonio García-Ranea and James Richard Perkins

Ligand access may be as important as binding for xenobiotic selection of AhR

Dániel Szöllosi, Gergely Gyimesi, Csaba Magyar and Tamas Hegedus

Genomic data modeling for interoperability and next generation genomic data management

Stefano Ceri, Abdulrahman Kaitoua, Pietro Pinoli and Marco Masseroli

Exploring outlier documents to investigate potential links between gut microbiota and Alzheimer's disease

Bojan Cestnik, Elsa Fabretti, Donatella Gubiani, Nada Lavrac and Tanja Urbancic

Integrative meta-analysis of pharmacological HDAC inhibition identifies complex epigenomic interactions with novel links to human disease

Assam El-Osta

Session: Virtual Presentation

Chairman: Dr. Ignacio Rojas and Dr. Francisco Ortuño

Augmented Reality Card System for Emergency Medical Services

Jorge Salvador Ierache, Santiago Igarza, Nicolas Verdicchio, Nicolás Duarte Duarte, Nahuel Mangiarua, Diego Sanz, Jonathan Barth, Cristian Montalvo and Facundo Petrolo

In silico studies of NSAIDs towards COX-1 and COX-2 inhibition. The correlation between IC50 values and binding energy with ADMET parameters

Chrysoula Mikra, Georgios Rossos, Sotirios Hadjikakou and Nikolaos Kourkoumelis

Evaluation of Disambiguation Strategies on Biomedical Text Categorization

Mohammed Rais and Abdelmonaime Lachkar

The Use of Miyazawa-Jernigan Residue Contact Potential in Analyses of Molecular Interaction and Recognition of Complementary Peptides

Nikola Štambuk, Paško Konjevoda, Zoran Manojlovic and Renata Novak-Kujundžic

Miyazawa-Jernigan Contact Potentials and Carter-Wolfenden Vapour to Cyclohexane and Water to Cyclohexane Scales as Parameters for Calculating Amino Acid Pair Distances

Nikola Štambuk, Paško Konjevoda and Zoran Manojlovic

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